Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for the relative quantification of the methylation of cytosine bases in DNA samples, said method comprising the steps of:

a) chemically reacting a genomic DNA sample with a reagent, wherein 5-methylcytosine and cytosine react differently and these thus show a different base pairing behavior in the DNA duplex after the reaction;

b) then, amplifying the chemically reacted DNA sample, said amplifying step comprising the use of a fluorescently labeled dCTP or dGTP derivative to yield amplified products;

c) then, spatially separating the amplified products from each other; ~~and~~

d) then, quantitatively measuring the fluorescence of the separated amplified products; and

e) then, determining from the measured fluorescence the relative number of methylated cytosine bases that were present in the DNA sample prior to step a).

2. (Previously presented) The method according to claim 1, further characterized in that the amplified DNA sample is hybridized to one or more immobilized oligomers, whereby the immobilized oligomers hybridize at least to one of the primers used in the amplification step or sequences complementary thereto in order to achieve the spatial separation.

3. (Original) The method according to claim 1, further characterized in that the amplified products from step (b) are separated by electrophoresis or chromatography.

4. (Original) The method according to claim 3, further characterized in that the separation is achieved by capillary gel electrophoresis.

5. (Original) The method according to claim 3, further characterized in that the separation is achieved by high pressure liquid chromatography (HPLC).

6. (Previously presented) The method according to claim 1, further characterized in that a bisulfite solution is used in step (a) as the reagent.

7. (Original) The method according to claim 1, further characterized in that PCR is used in step (b) for the amplification.

8. (Original) The method according to claim 1, further characterized in that in step (b) the fluorescently labeled dCTP or dGTP derivative is Cy3-dCTP, Cy5-dCTP, Cy3-dGTP or Cy5-dGTP.

9. (Original) The method according to claim 1, further characterized in that the fluorescent dyes Cy3 and/or Cy5 are used as the label.

10. (Previously presented) The method according to claim 2, further characterized in that an array of oligomers complementary or identical to the primers of step (b) is used for the hybridizing of the amplified products in step (c).

11. (Original) The method according to claim 1, further characterized in that the amplification of several DNA segments in step (b) is conducted simultaneously.

12. (Currently amended) The method according to claim 1, wherein ~~the values measured in step (d) are equilibrated~~ said determining step comprises comparing the fluorescence intensity from each of the separated amplified products with the fluorescence intensity of other, analogously treated DNA samples ~~and in this way information is obtained on~~ in order to ascertain the relative degree of methylation ~~of different tissues or different cell samples~~ that was present in the DNA sample.

13. (Previously presented) The method according to claim 1, further characterized in that fluorescently labeled primers are used in the amplification step, wherein their fluorescent labeling is different from that of the dCTP or dGTP derivatives.

14. (Currently amended) A method for the relative quantification of the methylation of cytosine bases in DNA samples, said method consisting of the steps of:

a) chemically reacting a genomic DNA sample with a reagent, wherein 5-methylcytosine and cytosine react differently and these thus show a different base pairing behavior in the DNA duplex after the reaction;

b) then, amplifying the chemically reacted DNA sample, wherein said amplifying step comprises the use of a fluorescently labeled dCTP or dGTP derivative to yield amplified products;

c) then, spatially separating the amplified products from each other; ~~and~~

d) then, quantitatively measuring the fluorescence of the separated amplified products; and.

e) then, determining from the measured fluorescence the relative number of methylated cytosine bases that were present in the DNA sample prior to step a).